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<110> Ullrich, Axel
      Aoki, Naohito
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      Wang, Hong Yang
      Chen, Zhengjun
      Nayler, Oliver
      Kharitonenkov, Alexei
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Arg Ser His Ser Ser Ala Arg Glu Gln Lys Arg Cys Arg Tyr Asp His
35 40 45

Ser Lys Thr Thr Asp Ser Tyr Tyr Leu Glu Ser Arg Ser Ile Asn Glu
50 60

Lys Ala Tyr His Ser Arg Arg Tyr Val Asp Glu Tyr Arg Asn Asp Tyr 65 70 75 80

Met Gly Tyr Glu Pro Gly His Pro Tyr Gly Glu Pro Gly Ser Arg Tyr 85 90 95

Gln Met His Ser Ser Lys Ser Ser Gly Arg Ser Gly Arg Ser Ser Tyr 100 105 110

Lys Ser Lys His Arg Ser Arg His His Thr Ser Asp His His Ser His 115 120 125

Gly His Ser His Arg Arg Lys Arg Ser Arg Ser Val Glu Asp Asp Glu 130 135 140

Glu Gly His Leu Ile Cys Gln Ser Gly Asp Val Leu Ser Ala Arg Tyr 145 150 155 160

Glu Ile Val Asp Thr Leu Gly Glu Gly Ala Phe Gly Lys Val Val Glu
165 170 175

Cys Ile Asp His Lys Val Gly Gly Arg Arg Val Ala Val Lys Ile Val 180 185 190

Lys Asn Val Asp Arg Tyr Cys Glu Ala Ala Gln Ser Glu Ile Gln Val 195 200 205

Leu Glu His Leu Asn Thr Thr Asp Pro His Ser Thr Phe Arg Cys Val 210 215 220

Gln Met Leu Glu Trp Phe Glu His Arg Gly His Ile Cys Ile Val Phe 225 230 235 240

Glu Leu Leu Gly Leu Ser Thr Tyr Asp Phe Ile Lys Glu Asn Ser Phe 245 250 255

Leu Pro Phe Arg Met Asp His Ile Arg Lys Met Ala Tyr Gln Ile Cys 260 265 270 Lys Ser Val Asn Phe Leu His Ser Asn Lys Leu Thr His Thr Asp Leu 275 280 285

Lys Pro Glu Asn Ile Leu Phe Val Lys Ser Asp Tyr Thr Glu Ala Asn 290 295 300

Pro Lys Met Lys Arg Asp Glu Arg Thr Ile Val Asn Pro Asp Ile Lys 305 310 315 320

Val Val Asp Phe Gly Ser Ala Thr Tyr Asp Asp Glu His His Ser Thr 325 330 335

Leu Val Ser Thr Arg His Tyr Arg Ala Pro Glu Val Ile Leu Ala Leu 340 345 350

Gly Trp Ser Gln Pro Cys Asp Val Trp Ser Ile Gly Cys Ile Leu Ile 355 360 365

Glu Tyr Tyr Leu Gly Phe Thr Val Phe Pro Thr His Asp Ser Arg Glu 370 . 375 380

His Leu Ala Met Met Glu Arg Ile Leu Gly Pro Leu Pro Lys His Met 385 390 395 400

Ile Gln Lys Thr Arg Lys Arg Arg Tyr Phe His His Asp Arg Leu Asp 405 410 415

Trp Asp Glu His Ser Ser Ala Gly Arg Tyr Val Ser Arg Arg Cys Lys 420 425 430

Pro Leu Lys Glu Phe Met Leu Ser Gln Asp Ala Glu His Glu Phe Leu 435 440 445

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His Thr

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Ser Phe Leu Glu Gln Gln Glu Ala Arg Asp His Arg Lys Gly Ala Ile
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Leu Ala Arg Glu Phe Ser Asp Ile Lys Ala Arg Ser Val Ala Trp Lys
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act gaa ggt gtg tgc tcc act aaa gcc ggc agt cag cag gga aac tca
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Thr Glu Gly Val Cys Ser Thr Lys Ala Gly Ser Gln Gly Asn Ser
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aag aag aac cgc tac aaa gac gtg gta ccg tat gat gag acg aga gtc
Lys Lys Asn Arg Tyr Lys Asp Val Val Pro Tyr Asp Glu Thr Arg Val
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Asn Phe Ile Arg Gly Thr Asp Gly Ser Gln Ala Tyr Ile Ala Thr Gln
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gga ccc ctg cct cac act ctg ttg gac ttc tgg cgc ctg gtt tgg gag
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Gly Pro Leu Pro His Thr Leu Leu Asp Phe Trp Arg Leu Val Trp Glu
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		gaa cgc Glu Arg	Tyr T									486
	Pro Phe	tgc ato Cys Ile										534
		agg acc Arg Thr 175	Leu G									582
		g cta cag n Leu Gln 190										630
		cac att His Ile										678
		a cct gga / Pro Gly	Pro Le	-								726
	Thr Gly	gtc ttg Val Leu										774
		a atc cca f Ile Pro 255										822
		a cag cga s Gln Arg 270										870
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	_	ctc tac Leu Tyr	Gln As		_			-	_			966
	Asp Ser	c tog tod Ser Ser										1014
		g ggt ggc 1 Gly Gly 335										1062

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	n Pro Ser			gaa gta aca gat gga Glu Val Thr Asp Gly 425	1302
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			tgg aca cgg Trp Thr Arg 450	gtg taatgagtgc Val	1396
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<213> Rattus rattus

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Ile Lys Ala Arg Ser Val Ala Trp Lys Thr Glu Gly Val Cys Ser Thr 35 40 45

Lys Ala Gly Ser Gln Gln Gly Asn Ser Lys Lys Asn Arg Tyr Lys Asp 50 55 60

Val Val Pro Tyr Asp Glu Thr Arg Val Ile Leu Ser Leu Leu Gln Glu 65 70 75 80

Glu Gly His Gly Asp Tyr Ile Asn Ala Asn Phe Ile Arg Gly Thr Asp 85 90 95

Gly Ser Gln Ala Tyr Ile Ala Thr Gln Gly Pro Leu Pro His Thr Leu 100 105 110

Leu Asp Phe Trp Arg Leu Val Trp Glu Phe Gly Ile Lys Val Ile Leu 115 120 125

Met Ala Cys Gln Glu Thr Glu Asn Gly Arg Arg Lys Cys Glu Arg Tyr 130 135 140

Trp Ala Gln Glu Arg Glu Pro Leu Gln Ala Gly Pro Phe Cys Ile Thr
145 150 155 160

Leu Thr Lys Glu Thr Ala Leu Thr Ser Asp Ile Thr Leu Arg Thr Leu 165 170 175

Gln Val Thr Phe Gln Lys Glu Ser Arg Pro Val His Gln Leu Gln Tyr 180 185 190

Met Ser Trp Pro Asp His Gly Val Pro Ser Ser Ser Asp His Ile Leu 195 200 205

Thr Met Val Glu Glu Ala Arg Cys Leu Gln Gly Leu Gly Pro Gly Pro 210 220

Leu Cys Val His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Leu Cys 225 230 235 240

Ala Val Asp Tyr Val Arg Gln Leu Leu Leu Thr Gln Thr Ile Pro Pro 245 250 255

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cgacctccaa cc atg gcc cgt gcc cag gcg ctc gtg ctg gca ctc acc ttc 171

Met Ala Arg Ala Gln Ala Leu Val Leu Ala Leu Thr Phe

1 5 10

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												cct Pro				315
												gtc Val				363
												cag Gln 90				411
												ctg Leu				459
												gtt Val				507
												cac His				555
												ccc Pro				603
_		_			_					_	-	agg Arg 170				651
												gca Ala				699
												ggc Gly				747
												caa Gln				795
												gcg Ala				843

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gcc Ala	gag Glu 255	cag Gln	gac Asp	ctg Leu	tac Tyr	cgc Arg 260	tgt Cys	gtg Val	tcc Ser	cag Gln	gcc Ala 265	ccg Pro	cgc Arg	ggc	ggc Gly	939
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		att Ile														2955
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cgt Arg	atg Met	gtg Val 960	tgg Trp	cag Gln	gag Glu	cac His	tgt Cys 965	tcc Ser	agc Ser	atc Ile	gtc Val	atg Met 970	atc Ile	acc Thr	aag Lys	3051
ctg Leu	gtc Val 975	gag Glu	gtg Val	ggc Gly	agg Arg	gtg Val 980	aaa Lys	tgc Cys	tca Ser	cgg Arg	tac Tyr 985	tgg Trp	ccg Pro	gag Glu	gac Asp	3099
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		cgg Arg					Gln					Ala				3243
	Gly	gtc Val 1040				Āla					Āla					3291
Val	_	gcc Ala			Pro		_			Pro						3339
	Ala	ggc Gly		Gly					Tyr					Val		3387
		atg Met	Āla					Val					Asn			3435
		ctc Leu					Val					Thr				3483
		-	1105													

acc acc atc cct gtc ag Thr Thr Ile Pro Val Se 1135	gt gag ttc aag g er Glu Phe Lys A 1140	cc acc tac aag la Thr Tyr Lys 1145	gag atg atc 35° Glu Met Ile	79
cgc att gat cct cag ag Arg Ile Asp Pro Gln Se 1150 115	er Asn Ser Ser G	ag ctg cgg gaa ln Leu Arg Glu 1160	gag ttc cag 362 Glu Phe Gln 1165	27
acg ctg aac tcg gtc ac Thr Leu Asn Ser Val Tl 1170		sp Val Glu Glu		75
gcc ctg ttg ccc cgg as Ala Leu Leu Pro Arg As 1185		sn Arg Ser Met		23
ccg ccc gac cgc tgc ct Pro Pro Asp Arg Cys Le 1200				71
aac aac tac att aat go Asn Asn Tyr Ile Asn A 1215				19
gcc ttc atg gtg acc ct Ala Phe Met Val Thr Le 1230 123	eu His Pro Leu G			67
tgg cgg ctg gtc tac ga Trp Arg Leu Val Tyr As 1250	at tac ggg tgc a sp Tyr Gly Cys T 12	hr Ser Ile Val	atg ctc aac 39 Met Leu Asn 1260	15
cag ctg aac cag tcc a Gln Leu Asn Gln Ser A 1265		ro Cys Leu Gln		63
gag cca ggc cgg cag cag Glu Pro Gly Arg Gln G 1280				11
ggc aca gct gat gaa ga Gly Thr Ala Asp Glu As 1295	ac tta gtg gct c sp Leu Val Ala A 1300	ga gtc ttc cgg rg Val Phe Arg 1305	gtg cag aac 409 Val Gln Asn	59
atc tct cgg ttg cag ga Ile Ser Arg Leu Gln G 1310 13	lu Gly Asp Leu L			07
ctg cgc tgg tct gca ta Leu Arg Trp Ser Ala T 1330		ro Asp Ser Lys		55
ttg cac ctg ctg gct ga Leu His Leu Leu Ala G 1345		rp Gln Ala Glu		03

ggg cgc acc atc gtg cac tgc cta aac ggg gga gga cgc agc ggc acc 425 Gly Arg Thr Ile Val His Cys Leu Asn Gly Gly Gly Arg Ser Gly Thr 1360 1365 1370	1
ttc tgc gcc tgc gcc acg gtc ctg gag atg atc cgc tgc cac aac ttg 4299 Phe Cys Ala Cys Ala Thr Val Leu Glu Met Ile Arg Cys His Asn Leu 1375 1380 1385	9
gtg gac gtt ttc ttt gct gcc caa acc ctc cgg aac tac aaa ccc aac 434° Val Asp Val Phe Phe Ala Ala Gln Thr Leu Arg Asn Tyr Lys Pro Asn 1390 1395 1400 1405	7
atg gtg gag acc atg gat cag tac cac ttt tgc tac gat gtg gcc ctg 4399 Met Val Glu Thr Met Asp Gln Tyr His Phe Cys Tyr Asp Val Ala Leu 1410 1415 1420	5
gag tac ttg gag ggg ctg gag tca aga tagcggggcc ctggcctggg 4444 Glu Tyr Leu Glu Gly Leu Glu Ser Arg 1425 1430	2
gcacccactg cacactcagg gccagaccca ccatcctgga ctggcgagga agatcagtgc 450	2
ctcctgctct gcccaaacac actcccatgg ggcaagcact ggagtggatg ctgggctatc 456	2
ttgctccccc ttccactgtg ggcagggcct ttcgcttgtc ccatgggcgg gtggtgggcc 462	2
aaggaggage ttagcaagte tgeageceae eeceaeetee atagggteet geaggeetgt 468	2
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gactcaggcc aagggggttg gcaggatcct gggttttggc agggatgagt gaggccctgc 480	2
agagagcate ecaggecaag gtteecaete ageetgeeee etetgeatgt gggtagagga 486	2
tgtactggga cttggcattt aggattccat ctgggggacc ccctgaaggt ccccccaag 492	2
caggteteaa ttetgatage cagtggggea caeteaetgt ceteeceagg ggaactgeag 498	2
cgccctcctc cccactgccc cctgcagccc ctgagatatt ttgctcacta tccctcccca 504	2
cttgcttccc tgatatgtgc tctgacttcc ctgaaccagg atctgcctat tactgctgtc 510	2
ccatgggggg ctccttccct gcctgaccca ctgttgcaga atgaagtcac ctcgccccc 516	2
tetteettta atetteagge eteaetggee tgteetgete agettgggee agtgacaate 522	2
tgcaaggctg aacaacagcc cctggggttg aggcccctgt ggctcctggt caggctgccc 528	2
gttgtgggga ggggcagtgt tagagcaggg ctggtcatac cctctggagt tcagagcaag 534	2
aggtaggacc agtgcttttt tgtttctttt gttatttttg gttgggtggg tgggaaggtc 540	2
totttaaaat ggggcaggco acacccccat toogtgcotc aatttoocca totgtaaact 546	2
gtagatatga ctactgacct acctcgcagg gggctgtggg gaggcataag ctgatgtttg 552	2
taaagcgctt tgtaaataaa cgtgctctct gaatgccaaa aaaaaaaaa caaaaaaaa 558	1

- <210> 34
- <211> 1430
- <212> PRT
- <213> Unknown Organism
- <223> Description of Unknown Organism: Mammalian PCP-2
 sequence

<400> 34

- Met Ala Arg Ala Gln Ala Leu Val Leu Ala Leu Thr Phe Gln Leu Cys

 1 10 15
- Ala Pro Glu Thr Glu Thr Pro Ala Ala Gly Cys Thr Phe Glu Glu Ala
 20 25 30
- Ser Asp Pro Ala Val Pro Cys Glu Tyr Ser Gln Ala Gln Tyr Asp Asp 35 40 45
- Phe Gln Trp Glu Gln Val Arg Ile His Pro Gly Thr Arg Ala Pro Ala 50 55 60
- Asp Leu Pro His Gly Ser Tyr Leu Met Val Asn Thr Ser Gln His Ala 65 70 75 80
- Pro Gly Gln Arg Ala His Val Ile Phe Gln Ser Leu Ser Glu Asn Asp 85 90 95
- Thr His Cys Val Gln Phe Ser Tyr Phe Leu Tyr Ser Arg Asp Gly Thr 100 105 110
- Gly Gly Thr Leu Arg Val Tyr Val Arg Val Asn Gly Gly Pro Leu Ala 115 120 125
- Ser Ala Val Trp Asn Met Thr Gly Ser His Gly Arg Gln Trp His Gln 130 135 140
- Ala Glu Leu Ala Val Ser Thr Phe Trp Pro Asn Glu Tyr Gln Val Leu 145 150 155 160
- Phe Glu Ala Leu Ile Ser Pro Asp Arg Gly Tyr Met Gly Leu Asp 165 170 175
- Asp Ile Leu Leu Ser Tyr Pro Cys Ala Lys Ala Pro His Phe Ser 180 185 190
- Arg Leu Gly Asp Val Glu Val Asn Ala Gly Gln Asn Ala Ser Phe Gln 195 200 205
- Cys Met Ala Ala Gly Glu Pro Met Arg Gln Arg Phe Leu Leu Gln Arg 210 215 220
- Gln Ser Gly Ala Leu Val Pro Ala Gly Ala Phe Gly Thr Ser Ala Thr 225 230 235 240
- Gly Phe Leu Ala Thr Phe Pro Leu Ala Ala Val Ser Arg Ala Glu Gln
 245 250 255

- Asp Leu Tyr Arg Cys Val Ser Gln Ala Pro Arg Gly Gly Val Ser Asn 260 265 270
- Phe Pro Glu Leu Ile Val Lys Glu Pro Pro Thr Pro Ile Ala Pro Pro
 275 280 285
- Gln Leu Leu Arg Ala Gly Pro Thr Tyr Leu Ile Ile Gln Leu Asn Thr 290 295 300
- Asn Ser Ile Ile Gly Asp Gly Pro Ile Val Arg Lys Glu Ile Glu Tyr 305 310 315 320
- Arg Met Ala Arg Gly Pro Trp Ala Glu Val His Ala Val Ser Leu Gln
 325 330 335
- Thr Tyr Lys Leu Trp His Leu Asp Pro Asp Thr Asp Tyr Glu Ile Ser 340 345 350
- Val Leu Leu Thr Arg Pro Gly Asp Gly Gly Thr Gly Arg Trp Ala Thr 355 360 365
- Pro His Gln Pro His Gln Met Arg Arg Ala His Glu Gly Pro Lys Gly 370 375 380
- Leu Ala Phe Ala Glu Ile Gln Ala Arg Gln Leu Thr Leu Gln Trp Glu 385 390 395 400
- Pro Leu Gly Tyr Asn Val Thr Arg Cys His Thr Tyr Thr Val Ser Leu 405 410 415
- Cys Tyr His Tyr Thr Leu Gly Ser Ser His Asn Gln Thr Ile Arg Glu
 420 425 430
- Cys Val Lys Thr Glu Gln Gly Val Ser Arg Tyr Thr Ile Lys Asn Leu 435 440 445
- Leu Pro Tyr Arg Asn Val His Val Arg Leu Val Leu Thr Asn Pro Glu 450 455 460
- Gly Arg Lys Glu Gly Lys Glu Val Thr Phe Gln Thr Asp Glu Asp Val 465 470 475 480
- Pro Ser Gly Ile Ala Ala Glu Ser Leu Thr Phe Thr Pro Leu Glu Asp 485 490 495
- Met Ile Phe Leu Lys Trp Glu Glu Pro Gln Glu Pro Asn Gly Leu Ile 500 505 510
- Thr Gln Tyr Glu Ile Ser Tyr Gln Ser Ile Glu Ser Ser Asp Pro Ala
 515 520 525
- Val Asn Val Pro Gly Pro Arg Arg Thr Ile Ser Lys Leu Arg Asn Glu 530 535 540
- Thr Tyr His Val Phe Ser Asn Leu His Pro Gly Thr Thr Tyr Leu Phe 545 550 555 560

- Ser Val Arg Ala Arg Thr Gly Lys Gly Phe Gly Gln Ala Ala Leu Thr 565 570 575
- Glu Ile Thr Thr Asn Ile Ser Ala Pro Ser Phe Asp Tyr Ala Asp Met 580 585 590
- Pro Ser Pro Leu Gly Glu Ser Glu Asn Thr Ile Thr Val Leu Leu Arg 595 600 605
- Pro Ala Gln Gly Arg Gly Ala Pro Ile Ser Val Tyr Gln Val Ile Val 610 615 620
- Glu Glu Glu Arg Ala Arg Gly Cys Gly Gly Thr Arg Trp Thr Gly Leu 625 630 635 640
- Leu Pro Ser Ala Ile Asp Leu Arg Gly Gly Ala Gly Pro Arg Leu Val 645 650 655
- His Tyr Phe Gly Ala Glu Leu Ala Ala Ser Ser Leu Pro Glu Ala Met 660 665 670
- Pro Phe Thr Val Gly Asp Asn Gln Thr Tyr Arg Gly Phe Trp Asn Pro 675 680 685
- Pro Leu Glu Pro Arg Lys Ala Tyr Leu Ile Tyr Phe Gln Ala Ala Ser 690 695 700
- His Leu Lys Gly Glu Thr Arg Leu Asn Cys Ile Arg Ile Ala Arg Lys 705 710 715 720
- Ala Ala Cys Lys Glu Ser Lys Arg Pro Leu Glu Val Ser Gln Arg Ser 725 730 735
- Glu Glu Met Gly Leu Ile Leu Gly Ile Cys Ala Gly Gly Leu Ala Val 740 745 750
- Leu Ile Leu Leu Gly Ala Ile Ile Val Ile Ile Arg Lys Gly Lys
 755 760 765
- Pro Val Asn Met Thr Lys Ala Thr Val Asn Tyr Arg Gln Glu Lys Thr 770 775 780
- His Met Ile Ser Ala Val Asp Arg Ser Phe Thr Asp Gln Ser Thr Leu 785 790 795 800
- Gln Glu Asp Glu Arg Leu Gly Leu Ser Phe Met Asp Thr His Gly Tyr 805 810 815
- Ser Thr Arg Gly Asp Gln Arg Ser Gly Gly Val Thr Glu Ala Ser Ser 820 825 830
- Leu Leu Gly Gly Ser Pro Arg Arg Pro Cys Gly Arg Lys Gly Ser Pro 835 840 845
- Tyr His Thr Gly Gln Leu His Pro Ala Val Arg Val Ala Asp Leu Leu 850 860

- Gln His Ile Asn Gln Met Lys Thr Ala Glu Gly Tyr Gly Phe Lys Gln 865 870 875 880
- Glu Tyr Glu Ser Phe Phe Glu Gly Trp Asp Ala Thr Lys Lys Lys Asp 885 890 895
- Lys Val Lys Gly Ser Arg Gln Glu Pro Met Pro Ala Tyr Asp Arg His 900 905 910
- Arg Val Lys Leu His Pro Met Leu Gly Asp Pro Asn Ala Asp Tyr Ile 915 920 925
- Asn Ala Asn Tyr Ile Asp Gly Tyr His Arg Ser Asn His Phe Ile Ala 930 935 940
- Thr Gln Gly Pro Lys Pro Glu Met Val Tyr Asp Phe Trp Arg Met Val 945 950 955 960
- Trp Gln Glu His Cys Ser Ser Ile Val Met Ile Thr Lys Leu Val Glu 965 970 975
- Val Gly Arg Val Lys Cys Ser Arg Tyr Trp Pro Glu Asp Ser Asp Thr 980 985 990
- Tyr Gly Asp Ile Lys Ile Met Leu Val Lys Thr Glu Thr Leu Ala Glu
 995 1000 1005
- Tyr Val Val Arg Thr Phe Ala Leu Glu Arg Arg Gly Tyr Ser Ala Arg 1010 1015 1020
- His Glu Val Arg Gln Ser His Phe Thr Ala Trp Pro Glu His Gly Val 1025 1030 1035 1040
- Pro Tyr His Ala Thr Gly Leu Leu Ala Phe Ile Arg Arg Val Lys Ala 1045 1050 1055
- Ser Thr Pro Pro Asp Ala Gly Pro Ile Val Ile His Cys Ser Ala Gly 1060 1065 1070
- Thr Gly Arg Thr Arg Cys Tyr Ile Val Leu Asp Val Met Leu Asp Met 1075 1080 1085
- Ala Glu Cys Glu Gly Val Val Asp Ile Tyr Asn Cys Val Lys Thr Leu 1090 1095 1100
- Cys Ser Arg Arg Val Asn Met Ile Gln Thr Glu Glu Gln Tyr Ile Phe 1105 1110 1115 1120
- Ile His Asp Ala Ile Leu Glu Ala Cys Leu Cys Gly Glu Thr Thr Ile 1125 1130 1135
- Pro Val Ser Glu Phe Lys Ala Thr Tyr Lys Glu Met Ile Arg Ile Asp 1140 1145 1150
- Pro Gln Ser Asn Ser Ser Gln Leu Arg Glu Glu Phe Gln Thr Leu Asn 1155 1160 1165

Ser Val Thr Pro Pro Leu Asp Val Glu Glu Cys Ser Ile Ala Leu Leu 1170 1175 1180

Pro Arg Asn Arg Asp Lys Asn Arg Ser Met Asp Val Leu Pro Pro Asp 1185 1190 1195 1200

Arg Cys Leu Pro Phe Leu Ile Ser Thr Asp Gly Asp Ser Asn Asn Tyr 1205 1210 1215

Ile Asn Ala Ala Leu Thr Asp Ser Tyr Thr Arg Arg Ser Ala Phe Met 1220 1225 1230

Val Thr Leu His Pro Leu Gln Ser Thr Thr Pro Asp Phe Trp Arg Leu 1235 1240 1245

Val Tyr Asp Tyr Gly Cys Thr Ser Ile Val Met Leu Asn Gln Leu Asn 1250 1255 1260

Gln Ser Asn Ser Ala Trp Pro Cys Leu Gln Tyr Trp Pro Glu Pro Gly 1265 1270 1275 1280

Arg Gln Gln Tyr Gly Leu Met Glu Val Glu Phe Met Ser Gly Thr Ala 1285 1290 1295

Asp Glu Asp Leu Val Ala Arg Val Phe Arg Val Gln Asn Ile Ser Arg 1300 1305 1310

Leu Gln Glu Gly Asp Leu Leu Val Arg His Phe Gln Phe Leu Arg Trp 1315 1320 1325

Ser Ala Tyr Arg Asp Thr Pro Asp Ser Lys Lys Ala Phe Leu His Leu 1330 1335 1340

Leu Ala Glu Val Asp Lys Trp Gln Ala Glu Ser Gly Asp Gly Arg Thr 1345 1350 1355 1360

Ile Val His Cys Leu Asn Gly Gly Gly Arg Ser Gly Thr Phe Cys Ala 1365 1370 1375

Cys Ala Thr Val Leu Glu Met Ile Arg Cys His Asn Leu Val Asp Val 1380 1385 1390

Phe Phe Ala Ala Gln Thr Leu Arg Asn Tyr Lys Pro Asn Met Val Glu 1395 1400 1405

Thr Met Asp Gln Tyr His Phe Cys Tyr Asp Val Ala Leu Glu Tyr Leu 1410 1415 1420

Glu Gly Leu Glu Ser Arg 1425 1430

<210> 35

<211> 2810

<212> DNA

<213> Homo sapiens

<220> <221> CDS <222> (44)..(1417) <400> 35

gaatteggea egagegget ggaeettget egeeegegge gee atg age ege age Met Ser Arg Ser ctg gac tcg gcg cgg agc ttc ctg gag cgg ctg gaa gcg cgg ggc ggc Leu Asp Ser Ala Arg Ser Phe Leu Glu Arg Leu Glu Ala Arg Gly Gly 10 cgg gag ggg gca gtc ctc gcc ggc gag ttc agc gac atc cag gcc tgc 151 Arg Glu Gly Ala Val Leu Ala Gly Glu Phe Ser Asp Ile Gln Ala Cys 30 teg gee gee tgg aag get gae gge gtg tge tee ace gtg gee gge agt 199 Ser Ala Ala Trp Lys Ala Asp Gly Val Cys Ser Thr Val Ala Gly Ser 45 50 cqq cca qaq aac qtq aqq aag aac cgc tac aaa gac gtg ctg cct tat 247 Arq Pro Glu Asn Val Arq Lys Asn Arg Tyr Lys Asp Val Leu Pro Tyr 60 gat cag acg cga gta atc ctc tcc ctg ctc cag gaa gag gga cac agc 295 Asp Gln Thr Arg Val Ile Leu Ser Leu Leu Gln Glu Glu Gly His Ser gac tac att aat ggc aac ttc atc cgg ggc gtg gat gga agc ctg gcc Asp Tyr Ile Asn Gly Asn Phe Ile Arg Gly Val Asp Gly Ser Leu Ala tac att gcc acg caa gga ccc ttg cct cac acc ctg cta gac ttc tgg 391 Tyr Ile Ala Thr Gln Gly Pro Leu Pro His Thr Leu Leu Asp Phe Trp 105 110 aga ctg gtc tgg gag ttt ggg gtc aag gtg atc ctg atg gcc tgt cga 439 Arg Leu Val Trp Glu Phe Gly Val Lys Val Ile Leu Met Ala Cys Arg 120 125 487 gag ata gag aat ggg cgg aaa agg tgt gag cgg tac tgg gcc cag gag Glu Ile Glu Asn Gly Arg Lys Arg Cys Glu Arg Tyr Trp Ala Gln Glu 135 140 cag gag cca ctg cag act ggg ctt ttc tgc atc act ctg ata aag gag 535 Gln Glu Pro Leu Gln Thr Gly Leu Phe Cys Ile Thr Leu Ile Lys Glu 150 155 aaq tgq ctq aat gag gac atc atg ctc agg acc ctc aag gtc aca ttc 583 Lys Trp Leu Asn Glu Asp Ile Met Leu Arg Thr Leu Lys Val Thr Phe 165 cag aag gag too ogt tot gtg tac cag cta cag tat atg too tgg coa 631 Gln Lys Glu Ser Arg Ser Val Tyr Gln Leu Gln Tyr Met Ser Trp Pro 185 gac cgt ggg gtc ccc agc agt cct gac cac atg ctc gcc atg gtg gag 679

Asp	Arg	Gly	Val 200	Pro	Ser	Ser	Pro	Asp 205	His	Met	Leu	Ala	Met 210	Val	Glu	
						gga Gly										727
tgc Cys	agt Ser 230	gcg Ala	ggt Gly	tgt Cys	ggg gly	cga Arg 235	aca Thr	ggc Gly	gtc Val	ctg Leu	tgc Cys 240	acc Thr	gtg Val	gat Asp	tat Tyr	775
						acc Thr										823
						atg Met										871
						ttc Phe										919
						gcc Ala										967
						gac Asp 315										1015
_			_			cgc Arg									_	1063
						ggc Gly										1111
						cca Pro										1159
Gly aaa	acg Thr	999 Gly 375	acg Thr	gly ggg	gcg Ala	cgc Arg	agc Ser 380	gcg Ala	gag Glu	gag Glu	gcg Ala	ccg Pro 385	ctc Leu	tac Tyr	agc Ser	1207
						cag Gln 395										1255
						cgc Arg										1303
						gtg Val										1351

ggt ttc aac ctg cgc att ggg agg ccg aag ggt ccc cgg gac ccg cct 1399 Gly Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro Arg Asp Pro Pro 440 445 450

gct gag tgg acc cgg gtg taagtctaac gccagttcct gcctgttgcc 1447
Ala Glu Trp Thr Arg Val

tettgtgage teggaetget gatgeeegg tgetgetgag egeegtgeeg agaatggaaa 1507 cagtgggcct ggatcaaagt taaagtttct cagggtggga aatgtggggg ctttgcccaa 1567 tgactgtagc attcaaggct tgaggctgga ggaggtagct agggtatagt ggctggtgag 1627 gctgcacaga gcagattcaa gaaagaagat caggaagggg catgacccct gagttatgaa 1687 ggggagaagg gacagatgag cttccggaga ctgctctcct caccacacag cactagtcca 1747 tecteageae etgageetee eteaettgga caeteagggg accaeaaga gaagtggatg 1807 gacacttcgc catccaggca gaactaagcc aggcataacc acagccaagc agattaaccc 1867 caggcagacc gataaaaaga cctccagata ggcagacaga cagatggacc accaacctgg 1927 acagacagec aaagetteag agatacagte cacaggtgga caaagggate eecagecaga 1987 gagagagaga ccagccaaca gcttgataga ccagtgcagc cagagagacc accaaacaca 2047 gcccccaaaa gacagacatc tctgctagct ggacagccag gtggaccccc taagttagtc 2107 agattactag acagatataa acagatcccc tgctgaacag atatacagag ttctcagacc 2167 ccactccctc aggtgggctg gctggctgac agaccttctg gccagacaga ctcctaacca 2227 accagatgga etgecagaca ggeagacate agtecacatg gaateetgae ateccageca 2287 gccggccaga ctctcatctt gatgtcttga tggatggacc ccagctagtc agacatgatc 2347 ctccagattg acagacaagt cccccaaatg agtacacatc tccagctatt cagacagatg 2407 gagececage aaateaggae etatetagge agaececage cagaececeg ceagaeagae 2467 teceaaceag aetgaeeeet tgetgtteae aeageetgee gagtagetgg gaetaeaggt 2527 ctaatttttt tttttttaa gaaatgagtt tttgccatgt tgcccagact ggtcttgaac 2587 teceaacete aageaateet eetgeeteag eeteecaaag tgetgagatt acaggtgtga 2647 gccaccaggc tcagccccct aagatttgaa acactttaaa tggcccatgg tagggttcct 2707 gctaggataa aacattaagt ggctgttaaa agaaataaaa ggaggacacg tctctgtgca 2767 2810

<212> PRT <213> Homo sapiens

<400> 36

Met Ser Arg Ser Leu Asp Ser Ala Arg Ser Phe Leu Glu Arg Leu Glu 1 5 10 15

Ala Arg Gly Gly Arg Glu Gly Ala Val Leu Ala Gly Glu Phe Ser Asp 20 25 30

Ile Gln Ala Cys Ser Ala Ala Trp Lys Ala Asp Gly Val Cys Ser Thr 35 40 45

Val Ala Gly Ser Arg Pro Glu Asn Val Arg Lys Asn Arg Tyr Lys Asp 50 55 60

Val Leu Pro Tyr Asp Gln Thr Arg Val Ile Leu Ser Leu Leu Gln Glu 65 70 75 80

Glu Gly His Ser Asp Tyr Ile Asn Gly Asn Phe Ile Arg Gly Val Asp 85 90 95

Gly Ser Leu Ala Tyr Ile Ala Thr Gln Gly Pro Leu Pro His Thr Leu 100 105 110

Leu Asp Phe Trp Arg Leu Val Trp Glu Phe Gly Val Lys Val Ile Leu 115 120 125

Met Ala Cys Arg Glu Ile Glu Asn Gly Arg Lys Arg Cys Glu Arg Tyr 130 135 140

Trp Ala Gln Glu Gln Glu Pro Leu Gln Thr Gly Leu Phe Cys Ile Thr 145 150 155 160

Leu Ile Lys Glu Lys Trp Leu Asn Glu Asp Ile Met Leu Arg Thr Leu 165 170 175

Lys Val Thr Phe Gln Lys Glu Ser Arg Ser Val Tyr Gln Leu Gln Tyr 180 185 190

Met Ser Trp Pro Asp Arg Gly Val Pro Ser Ser Pro Asp His Met Leu 195 200 205

Ala Met Val Glu Glu Ala Arg Arg Leu Gln Gly Ser Gly Pro Glu Pro 210 215 220

Leu Cys Val His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Leu Cys 225 230 , 235 240

Thr Val Asp Tyr Val Arg Gln Leu Leu Leu Thr Gln Met Ile Pro Pro 245 250 255

Asp Phe Ser Leu Phe Asp Val Val Leu Lys Met Arg Lys Gln Arg Pro 260 265 270

Ala Ala Val Gln Thr Glu Glu Gln Tyr Arg Phe Leu Tyr His Thr Val 275 280 285

Ala Gln Met Phe Cys Ser Thr Leu Gln Asn Ala Ser Pro His Tyr Gln 290 295 300

Asn Ile Lys Glu Asn Cys Ala Pro Leu Tyr Asp Asp Ala Leu Phe Leu 305 310 315 320

Arg Thr Pro Gln Ala Leu Leu Ala Ile Pro Arg Pro Pro Gly Gly Val
325 330 335

Leu Arg Ser Ile Ser Val Pro Gly Ser Pro Gly His Ala Met Ala Asp 340 345 350

Thr Tyr Ala Glu Glu Gln Lys Arg Gly Ala Pro Ala Gly Ala Gly Ser 355 360 365

Gly Thr Gln Thr Gly Thr Gly Thr Gly Ala Arg Ser Ala Glu Glu Ala 370 375 380

Pro Leu Tyr Ser Lys Val Thr Pro Arg Ala Gln Arg Pro Gly Ala His 385 390 395 400

Ala Glu Asp Ala Arg Gly Thr Leu Pro Gly Arg Val Pro Ala Asp Gln
405 410 415

Ser Pro Ala Gly Ser Gly Ala Tyr Glu Asp Val Ala Gly Gly Ala Gln 420 425 430

Thr Gly Gly Leu Gly Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro 435 440 445

Arg Asp Pro Pro Ala Glu Trp Thr Arg Val 450 455

<210> 37

<211> 503

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Mammalian SIRP4 amino acid sequence

<400> 37

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Ser Val Ala Ala Gly 35 40 45

Glu Ser Ala Ile Leu His Cys Thr Val Thr Ser Leu Ile Pro Val Gly 50 60

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Ala Arg Glu Leu Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr 105 Pro Ala Asp Ala Gly Thr Tyr Cys Val Lys Phe Arg Lys Gly Ser Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile 200 His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln 220 210 215 Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg 230 235 Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu 250 245 Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys 265 Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu 280 285 Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn 300 Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser 315 Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro 345 Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu

360

365

Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala 370 375 380

Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys Ala 385 390 395 400

Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn Ala 405 410 415

Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu Asn 420 425 430

Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn Asn 435 440 445

His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser Glu 450 455 460

Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg Thr 465 470 475 480

Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala 485 490 495

Ser Val Gln Val Pro Arg Lys 500

<210> 38

<211> 398

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Mammalian SIRP1 amino acid sequence

<400> 38

Met Pro Val Pro Ala Ser Trp Pro His Leu Pro Ser Pro Phe Leu Leu
1 5 10 15

Met Thr Leu Leu Gly Arg Leu Thr Gly Val Ala Gly Glu Asp Glu 20 25 . 30

Leu Gln Val Ile Gln Pro Glu Lys Ser Val Ser Val Ala Ala Gly Glu
35 40 45

Ser Ala Thr Leu Arg Cys Ala Met Thr Ser Leu Ile Pro Val Gly Pro 50 60

Ile Met Trp Phe Arg Gly Ala Gly Ala Gly Arg Glu Leu Ile Tyr Asn 65 70 75 80

Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Leu Thr 85 90 95

Lys Arg Asn Asn Leu Asn Phe Ser Ile Ser Ile Ser Asn Ile Thr Pro 100 105 110

- Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser Pro 115 120 125
- Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg 130 135 140
- Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Val Arg Ala Thr 145 150 155 160
- Pro Glu His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro 165 170 175
- Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp 180 185 190
- Phe Gln Thr Asn Val Asp Pro Ala Gly Asp Ser Val Ser Tyr Ser Ile 195 200 205
- His Ser Thr Ala Arg Val Val Leu Thr Arg Gly Asp Val His Ser Gln 210 215 220
- Val Ile Cys Glu Met Ala His Ile Thr Leu Gln Gly Asp Pro Leu Arg 225 230 235 240
- Gly Thr Ala Asn Leu Ser Glu Ala Ile Arg Val Pro Pro Thr Leu Glu 245 250 255
- Val Thr Gln Gln Pro Met Arg Ala Glu Asn Gln Ala Asn Val Thr Cys 260 265 270
- Gln Val Ser Asn Phe Tyr Pro Arg Gly Leu Gln Leu Thr Trp Leu Glu 275 280 285
- Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Leu Ile Glu Asn 290 295 300
- Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Thr Cys 305 310 315 320
- Ala His Arg Asp Asp Val Val Leu Thr Cys Gln Val Glu His Asp Gly
 325 330 335
- Gln Gln Ala Val Ser Lys Ser Tyr Ala Leu Glu Ile Ser Ala His Gln 340 345 350
- Lys Glu His Gly Ser Asp Ile Thr His Glu Pro Ala Leu Ala Pro Thr 355 360 365
- Ala Pro Leu Leu Val Ala Leu Leu Gly Pro Lys Leu Leu Val 370 375 380
- Val Gly Val Ser Ala Ile Tyr Ile Cys Trp Lys Gln Lys Ala 385 390 395

<210> 39

<211> 495

<212> PRT

<213> Mus musculus

<400> 39

Pro Arg Pro Arg Lys Tyr His Ser Ser Glu Arg Gly Ser Arg Gly Ser 1 5 10 15

Tyr His Glu His Tyr Gln Ser Arg Lys His Lys Arg Arg Arg Ser Arg 20 25 30

Ser Trp Ser Ser Ser Ser Asp Arg Thr Arg Arg Arg Ala Arg Glu Asp
35 40 45

Ser Tyr His Val Arg Ser Arg Ser Ser Tyr Asp Asp His Ser Ser Asp 50 55 60

Arg Arg Leu Tyr Asp Arg Arg Tyr Cys Gly Ser Tyr Arg Arg Asn Asp 65 70 75 80

Tyr Ser Arg Asp Arg Gly Glu Ala Tyr Tyr Asp Thr Asp Phe Arg Gln 85 90 95

Ser Tyr Glu Tyr His Arg Glu Asn Ser Ser Tyr Arg Ser Gln Arg Ser 100 105 110

Ser Arg Arg Lys His Arg Arg Arg Arg Arg Ser Arg Thr Phe Ser 115 120 125

Arg Ser Ser Ser His Ser Ser Arg Arg Ala Lys Ser Val Glu Asp Asp 130 135 140

Ala Glu Gly His Leu Ile Tyr His Val Gly Asp Trp Leu Gln Glu Arg 145 150 155 160

Tyr Glu Ile Val Ser Thr Leu Gly Glu Gly Thr Ser Gly Arg Val Val 165 170 175

Gln Cys Ile Asp Arg Arg Val Gly Thr Arg Arg Val Leu Val Ile Ile 180 185 190

Lys Asn Val Glu Lys Tyr Lys Glu Ala Ala Arg Leu Glu Ile Asn Val 195 200 205

Leu Glu Lys Ile Asn Glu Lys Asp Pro Lys Asn Lys Asn Leu Cys Val 210 215 220

Gln Met Phe Asp Trp Phe Asp Tyr His Gly His Met Cys Ile Ser Phe 225 230 235 240

Glu Leu Leu Gly Leu Ser Thr Phe Asp Phe Leu Lys Asp Asn Asn Tyr
245 250 255

Leu Pro Tyr Pro Ile His Gln Val Arg His Met Ala Phe Gln Leu Cys 260 265 270

Gln Ala Val Lys Phe Leu His Asp Asn Lys Leu Thr His Thr Asp Leu 275 280 285

Lys Pro Glu Asn Ile Leu Phe Val Asn Ser Asp Tyr Glu Leu Thr Asn 290 295 300

Pro Leu Glu Lys Arg Asp Glu Arg Thr Ser Val Lys Ser Thr Ala Val 305 310 315 320

Arg Val Asp Phe Gly Ser Ala Thr Tyr Phe Asp His His Ser Thr 325 330 335

Leu Ile Ser Thr Arg His Tyr Arg Ala Pro Glu Val Ile Leu Glu Leu 340 345 350

Gly Trp Ser Gln Pro Cys Asp Val Trp Ser Ile Gly Cys Ile Phe Ile 355 360 365

Glu Tyr Val Leu Gly Phe Leu Val Gln Pro Thr His Asn Ser Arg Glu 370 375 380

His Leu Ala Met Glu Arg Ile Leu Gly Pro Val Pro Ser Arg Met Ile 385 390 395 400

Arg Lys Thr Arg Lys Gln Lys Tyr Phe Tyr Arg Gly Arg Leu Asp Trp
405 410 415

Asp Glu Asn Thr Ser Ala Gly Arg Tyr Val Arg Glu Asn Cys Lys Pro 420 425 430

Leu Arg Arg Tyr Leu Thr Ser Glu Ala Glu Asp His His Gln Leu Phe
435
440
445

Asp Leu Ile Glu Asn Met Leu Glu Tyr Glu Pro Ala Lys Arg Leu Thr 450 455 460

Leu Gly Glu Ala Leu Gln His Pro Phe Phe Ala Cys Leu Arg Thr Glu 465 470 475 480

Pro Pro Asn Thr Lys Leu Trp Asp Ser Ser Arg Asp Ile Ser Arg 485 490 495

<210> 40

<211> 484

<212> PRT

<213> Mus musculus

<400> 40

His Arg Cys Ser Lys Tyr Arg Ser Pro Glu Pro Asp Pro Tyr Leu Thr 1 5 10 15

Tyr Arg Trp Lys Glu Arg Arg Ser Asp Ser Arg Glu His Glu Gly Arg
20 25 30

Leu Arg Tyr Pro Ser Arg Lys Glu Pro Pro Pro Arg Ala Ser Ser Arg
35 40 45

- Glu Asp Ala Pro Tyr Arg Thr Arg Lys His Ala His His Cys His Lys 50 55 60
- Ile Arg Thr Arg Ser Cys Ser Ser Ala Ser Ser Arg Ser Gln Gln Ser 65 70 75 80
- Ser Lys Arg Ser Ser Arg Gly Glu Ser Arg Glu Arg Ala Pro Tyr Arg 85 90 95
- Thr Arg Lys His Ala His His Cys His Lys Arg Arg Thr Arg Ser Cys
 100 105 110
- Ser Ser Ala Ser Ser Arg Ser Gln Gln Ser Ser Lys Arg Ser Ser Arg 115 120 125
- Ser Val Glu Asp Asp Lys Glu Gly His Leu Val Cys Arg Ile Gly Ser 130 135 140
- Trp Leu Gln Glu Arg Tyr Glu Ile Val Gly Asn Leu Gly Glu Gly Thr
 145 150 155 160
- Phe Gly Lys Val Val Glu Cys Leu Asp His Ala Arg Gly Lys Ser Gln 165 170 175
- Val Ala Leu Lys Ile Ile Arg Asn Val Gly His Tyr Arg Glu Ala Ala 180 185 190
- Arg Leu Glu Ile Asn Val Leu Lys Lys Ile Lys Glu Lys Asp Lys Glu
 195 200 205
- Asn Lys Phe Leu Cys Val Leu Met Ser Asp Trp Asn Phe His Arg Gly 210 215
- Met Ile Cys Ala Val Glu Leu Leu Gly Lys Asn Thr Phe Glu Phe Leu 225 230 235 240
- Lys Glu Asn Asn Phe Gln Pro Tyr Pro Leu Pro His Val Arg His Met 245 250 255
- Ala Tyr Gln Leu Cys His Ala Leu Arg Phe Leu His Glu Asn Gln Leu 260 265 270
- Thr His Thr Asp Leu Lys Pro Glu Asn Ile Leu Phe Val Asn Ser Asp 275 280 285
- Glu Phe Glu Thr Leu Pro Lys Glu His Lys Ser Cys Glu Thr Lys Ser 290 295 300
- Val Lys Asp Thr Ser Ile Arg Asp Ala Gly Ser Ala Thr Tyr Asp Phe 305 310 315 320
- Glu His His Ser Thr Thr Val Ile Ala Thr Arg His Tyr Arg Pro Pro 325 330 335
- Glu Val Ile Leu Glu Leu Gly Trp Ala Gln Pro Cys Asp Val Trp Ser 340 345 350

Ile Gly Cys Ile Leu Phe Glu Tyr Tyr Arg Gly Phe Thr Leu Phe Gln 355 360 365

Thr His Asp Ser Lys Glu His Leu Ala Met Met Glu Lys Ile Leu Gly 370 375 380

Pro Ile Pro Ser His Met Ile His Arg Thr Arg Lys Gln Lys Tyr Phe 385 390 395 400

Tyr Lys Gly Gly Leu Val Trp Asp Glu Asn Ser Ser Asp Gly Arg Tyr 405 410 415

Val Lys Glu Asn Cys Lys Pro Leu Lys Ser Tyr Met Leu Gln Asp Ser 420 425 430

Leu Glu His Val Gln Leu Phe Asp Leu Met Arg Arg Met Leu Glu Phe 435 440 445

Asp Pro Ala Gln Arg Ile Thr Leu Ala Glu Ala Leu Leu His Pro Phe 450 455 460

Phe Ala Gly Leu Thr Pro Glu Glu Arg Ser Phe His Ser Ser Ser Arg 465 470 475 480

Asn Pro Ser Arg

<210> 41

<211> 481

<212> PRT

<213> Mus musculus

<400> 41

Met Arg His Ser Lys Arg Thr His Cys Pro Asp Trp Asp Ser Arg Glu
1 1 15

Ser Trp Gly His Glu Ser Tyr Ser Gly Ser His Lys Arg Lys Arg Arg 20 25 30

Ser His Ser Ser Thr Gln Glu Asn Arg His Cys Lys Pro His His Gln 35 40 45

Phe Lys Asp Ser Asp Cys His Tyr Leu Glu Ala Arg Cys Leu Asn Glu 50 55 60

Arg Asp Tyr Arg Asp Arg Tyr Ile Asp Glu Tyr Arg Asn Asp Tyr
65 70 75 80

Cys Glu Gly Tyr Val Pro Arg His Tyr His Arg Asp Val Glu Ser Thr 85 90 95

Tyr Arg Ile His Cys Ser Lys Ser Ser Val Arg Ser Arg Arg Ser Ser 100 105 110

Pro Lys Arg Lys Arg Asn Arg Pro Cys Ala Ser His Gln Ser His Ser 115 120 125

- Lys Ser His Arg Arg Lys Arg Ser Arg Ser Ile Glu Asp Asp Glu Glu 130 135 140
- Gly His Leu Ile Cys Gln Ser Gly Asp Val Leu Arg Ala Arg Tyr Glu 145 150 155 160
- Ile Val Asp Thr Leu Gly Glu Gly Ala Phe Gly Lys Val Val Glu Cys
 165 170 175
- Ile Asp His Gly Met Asp Gly Leu His Val Ala Val Lys 180 185 190
- Asn Val Gly Gly Tyr Arg Glu Ala Ala Arg Ser Glu Ile Gln Val Leu 195 200 205
- Glu His Leu Asn Ser Thr Asp Pro Asn Ser Val Phe Arg Cys Val Gln 210 215 220
- Met Leu Glu Trp Phe Asp His His Gly His Val Cys Ile Val Phe Glu 225 230 235 240
- Leu Leu Gly Leu Ser Thr Tyr Asp Phe Ile Lys Glu Asn Ser Phe Leu 245 250 255
- Pro Phe Gln Ile Asp His Ile Arg Gln Met Ala Tyr Gln Ile Cys Gln 260 265 270
- Ser Ile Asn Phe Leu His His Asn Lys Leu Thr His Thr Asp Leu Lys 275 280 285
- Pro Glu Asn Ile Leu Phe Val Lys Ser Asp Tyr Val Val Lys Asn Pro 290 295 300
- Ser Met Lys Arg Asp Glu Arg Thr Ile Leu Lys Pro Thr Asp Ile Lys 305 310 315 320
- Val Val Asp Phe Gly Ser Ala Thr Tyr Asp Asp Glu His His Ser Thr 325 330 335
- Leu Val Ser Thr Arg His Tyr Arg Ala Pro Glu Val Ile Leu Ala Leu 340 345 350
- Gly Trp Ser Gln Pro Cys Asp Val Trp Ser Ile Gly Cys Ile Leu Ile 355 360 365
- Glu Tyr Tyr Leu Gly Phe Thr Val Phe Gln Thr His Asp Ser Lys Glu 370 380
- His Leu Ala Met Met Glu Arg Ile Leu Gly Pro Ile Pro Ala His Met 385 390 395 400
- Ile Gln Lys Thr Arg Lys Arg Lys Tyr Phe His His Asn Gln Leu Asp 405 410 415
- Trp Asp Glu His Ser Ser Ala Gly Arg Tyr Val Arg Arg Arg Cys Lys
 420 425 430

Pro Leu Lys Glu Phe Met Leu Cys His Asp Glu Glu His Glu Lys Leu 435 440 445

Phe Asp Leu Val Arg Arg Met Leu Glu Tyr Asp Pro Ala Arg Arg Ile 450 455 460

Thr Leu Asp Glu Ala Leu Gln His Pro Phe Phe Asp Leu Leu Lys Arg 465 470 475 480

Lys